RAW SEQUENCE LISTING
ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH
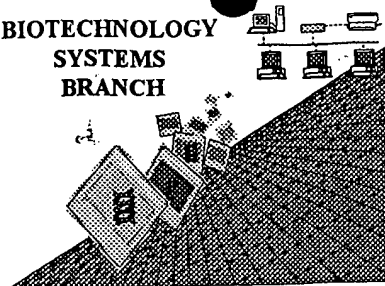
The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/734,583_

Source: _OIPE_

Date Processed by STIC: _9/6/2001_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov **or phone 703-306-4119 (R. Wax)**
PATENTIN 3.0 e-mail help: patin3help@uspto.gov **or phone 703-306-4119 (R. Wax)**

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.
Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

ERROR DETECTED **SUGGESTED CORRECTION** **SERIAL NUMBER:** 09/734,583

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1_____Wrapped Nucleics
      Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2_____Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3_____Misaligned Amino
      Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4_____Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5_____Variable Length

Sequence(s) ___ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6_____PatentIn 2.0
      "bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for **Artificial or Unknown sequences.**

7_____Skipped Sequences
      (OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
   (i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8_____Skipped Sequences
      (NEW RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9_____Use of n's or Xaa's
      (NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10_____Invalid <213>
      Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence. 2-9 (maybe more)

11_____Use of <220>

Sequence(s) 2-9 (maybe more) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12_____PatentIn 2.0
      "bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13_____Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

#6

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: **US/09/734,583**

DATE: 09/06/2001
TIME: 15:09:42

Does Not Comply
Corrected Diskette Needed

Input Set : **A:\87534-3000.txt**
Output Set: **N:\CRF3\09062001\I734583.raw**

```
 3 <110> APPLICANT: Hornik, Vered
 5 <120> TITLE OF INVENTION: CONFORMATIONALLY CONSTRAINED BACKBONE CYCLIZED SOMATOSTATIN
ANALOGS
 7 <130> FILE REFERENCE: 87534-3000
 9 <140> CURRENT APPLICATION NUMBER: 09/734,583
10 <141> CURRENT FILING DATE: 2000-12-13
12 <160> NUMBER OF SEQ ID NOS: 10
14 <170> SOFTWARE: PatentIn version 3.1
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 14
18 <212> TYPE: PRT
19 <213> ORGANISM: mammalian
21 <400> SEQUENCE: 1
23 Ala Gly Cys Lys Asn Phe Phe Trp Lys Thr Phe Thr Ser Cys
24 1               5                   10
27 <210> SEQ ID NO: 2
28 <211> LENGTH: 6
29 <212> TYPE: PRT
30 <213> ORGANISM: Artificial peptide
32 <220> FEATURE:
33 <221> NAME/KEY: DISULFIDE BRIDGE
34 <222> LOCATION: (1)..(1)
35 <223> OTHER INFORMATION: Cys residues at amino acid positions 1 and 6 form a disulfide
36          e
39 <220> FEATURE:
40 <221> NAME/KEY: MOD_RES
41 <222> LOCATION: (3)..(3)
42 <223> OTHER INFORMATION: The Trp residue is the D isomer
45 <400> SEQUENCE: 2
47 Cys Phe Trp Lys Thr Cys
48 1               5
51 <210> SEQ ID NO: 3
52 <211> LENGTH: 6
53 <212> TYPE: PRT
54 <213> ORGANISM: Artificial peptide
56 <220> FEATURE:
57 <221> NAME/KEY: MOD_RES
58 <222> LOCATION: (1)..(1)
59 <223> OTHER INFORMATION: N-Methyl
62 <220> FEATURE:
63 <221> NAME/KEY: MOD_RES
64 <222> LOCATION: (1)..(6)
65 <223> OTHER INFORMATION: cyclo
68 <220> FEATURE:
69 <221> NAME/KEY: MOD_RES
70 <222> LOCATION: (3)..(3)
71 <223> OTHER INFORMATION: The Trp residue is the D isomer
```

C--> (line 30)
W--> (line 33)
C--> (line 54)

invalid
see items 10 and 11 on Error summary sheet
1?
birdg *bridge?*
same error

74 <400> SEQUENCE: 3

```
        76 Ala Tyr Trp Lys Val Phe
        77 1                     5
        80 <210> SEQ ID NO: 4
        81 <211> LENGTH: 8
        82 <212> TYPE: PRT
C--> 83 <213> ORGANISM: Artificial Peptide
        85 <220> FEATURE:
        86 <221> NAME/KEY: MOD_RES
        87 <222> LOCATION: (1)..(1)
        88 <223> OTHER INFORMATION: The Phe residue is a D isomer
        91 <220> FEATURE:
        92 <221> NAME/KEY: MOD_RES
        93 <222> LOCATION: (8)..(8)
        94 <223> OTHER INFORMATION: The Thr residue ends with CH2OH
        97 <220> FEATURE:
W--> 98 <221> NAME/KEY: DISULFIDE BRIDGE                    bridge
        99 <222> LOCATION: (2)..(2)
       100 <223> OTHER INFORMATION: A disulfide bride is formed between Cys residues 2 and 7
       103 <220> FEATURE:
       104 <221> NAME/KEY: MOD_RES          4? Cys is at location 2
       105 <222> LOCATION: (2)..(2)
       106 <223> OTHER INFORMATION: The Trp residue is a D isomer
       109 <400> SEQUENCE: 4
       111 Phe Cys Phe Trp Lys Thr Cys Thr
       112 1                     5
       115 <210> SEQ ID NO: 5
       116 <211> LENGTH: 7
       117 <212> TYPE: PRT
C--> 118 <213> ORGANISM: Artificial Peptide
       120 <220> FEATURE:
W--> 121 <221> NAME/KEY: DISULFIDE
       122 <222> LOCATION: (2)..(2)
       123 <223> OTHER INFORMATION: A Disulfide Bridge is formed between the Cys residues at
position
       124        2 and 6
       127 <220> FEATURE:
       128 <221> NAME/KEY: MOD_RES
       129 <222> LOCATION: (1)..(1)
       130 <223> OTHER INFORMATION: The Phe residue is a D isomer
       133 <220> FEATURE:
       134 <221> NAME/KEY: MOD_RES
       135 <222> LOCATION: (4)..(4)
       136 <223> OTHER INFORMATION: The Trp residue is a D isomer
       139 <220> FEATURE:
       140 <221> NAME/KEY: MOD_RES                    residue
       141 <222> LOCATION: (7)..(7)
       142 <223> OTHER INFORMATION: The Thr resiude ends with N2H
       145 <400> SEQUENCE: 5
       147 Phe Cys Phe Trp Lys Cys Thr
       148 1                     5
```

```
    151 <210> SEQ ID NO: 6
    152 <211> LENGTH: 8
    153 <212> TYPE: PRT
C-->154 <213> ORGANISM: Artificial peptide
    156 <220> FEATURE:
    157 <221> NAME/KEY: MISC_FEATURE
    158 <222> LOCATION: (1)..(1)
    159 <223> OTHER INFORMATION: is a gamma amino butyric acid, diamino butyric acid, Gly,
beta-Al
    160      a, 5-amino pentanoic acid or amino hexanoic acid; Residue 1 is bi brrdged
    161      rdged to Residue 8; Residue 1 also begins with a hydrogen, or a m
    162      ono- or di- saccharide attached
    165 <220> FEATURE:
    166 <221> NAME/KEY: MISC_FEATURE
    167 <222> LOCATION: (2)..(2)
    168 <223> OTHER INFORMATION: is (D) or (L) Phe or Tyr
    171 <220> FEATURE:
    172 <221> NAME/KEY: MISC_FEATURE
    173 <222> LOCATION: (3)..(3)
    174 <223> OTHER INFORMATION: is (D) or (L)-Trp, or (L)-Phe, (D)- or (L)-1Nal or (D) or
(L)-2Na
    175      1, or Tyr
    178 <220> FEATURE:
    179 <221> NAME/KEY: MISC_FEATURE
    180 <222> LOCATION: (4)..(4)
    181 <223> OTHER INFORMATION: is (D) or (L)-Trp
    184 <220> FEATURE:
    185 <221> NAME/KEY: MISC_FEATURE
    186 <222> LOCATION: (5)..(5)
    187 <223> OTHER INFORMATION: is (D) or (L)-Lys
    190 <220> FEATURE:
    191 <221> NAME/KEY: MISC_FEATURE
    192 <222> LOCATION: (6)..(6)
    193 <223> OTHER INFORMATION: is Thr, Gly, Abu, Ser, Cys, Val, (D) or (L)-Ala, or (D)- or
(L)-A
    194      la, or Tyr
    197 <220> FEATURE:
    198 <221> NAME/KEY: MISC_FEATURE
    199 <222> LOCATION: (7)..(7)
    200 <223> OTHER INFORMATION: is (D) or (L)-Phe, or (D)- or (L)-Ala, Nle, or Cys;
    203 <220> FEATURE:
    204 <221> NAME/KEY: MISC_FEATURE
    205 <222> LOCATION: (8)..(8)
    206 <223> OTHER INFORMATION: is Gly, Val, Leu, (D) or (L)-Phe, or 1Nal or 2Nal; with a
termina
    207      l carboxy acid, amide or alcohol group.
    210 <400> SEQUENCE: 6
W-->212 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
    213 1                 5
    216 <210> SEQ ID NO: 7
    217 <211> LENGTH: 7
    218 <212> TYPE: PRT
C-->219 <213> ORGANISM: Artificial Peptide
```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/734,583

DATE: 09/06/2001
TIME: 15:09:42

Input Set : A:\87534-3000.txt
Output Set: N:\CRF3\09062001\I734583.raw

```
     221 <220> FEATURE:
     222 <221> NAME/KEY: MISC_FEATURE
     223 <222> LOCATION: (1)..(1)
     224 <223> OTHER INFORMATION: is (D)- or (L)-Phe, or (D)- or (L)-Ala; wherein Residue 1 is
brid
     225         ged to Residue 6 a bridging group composed of 1 to 5 methyl space
     226         rs connected to an amide, thioether, thioester, or disulfide, fol
     227         lowed by 1 to 5 methyl spacers
     230 <220> FEATURE:
     231 <221> NAME/KEY: MISC_FEATURE
     232 <222> LOCATION: (2)..(2)
     233 <223> OTHER INFORMATION: is Tyr or (D)- or (L)-Phe
     236 <220> FEATURE:
     237 <221> NAME/KEY: MISC_FEATURE
     238 <222> LOCATION: (3)..(3)
     239 <223> OTHER INFORMATION: is (D)- or (L)-Trp, (D)- or (L)-1Nal, or (D)- or (L)-2Nal
     242 <220> FEATURE:
     243 <221> NAME/KEY: MISC_FEATURE
     244 <222> LOCATION: (5)..(5)
     245 <223> OTHER INFORMATION: is Thr, Val, Ser, or Cys
     248 <220> FEATURE:
     249 <221> NAME/KEY: MISC_FEATURE
     250 <222> LOCATION: (6)..(6)
     251 <223> OTHER INFORMATION: is Gly or (D)- or (L)-Phe
     254 <220> FEATURE:
     255 <221> NAME/KEY: MISC_FEATURE
     256 <222> LOCATION: (7)..(7)
     257 <223> OTHER INFORMATION: is Thr, GABA, (D)- or (L)-1Nal, (D)- or (L)-2Nal, or (D)- or
(L
     258         )-Phe
     261 <400> SEQUENCE: 7
W--> 263 Xaa Xaa Xaa Lys Xaa Xaa Xaa
     264 1               5
     267 <210> SEQ ID NO: 8
     268 <211> LENGTH: 9
     269 <212> TYPE: PRT
C--> 270 <213> ORGANISM( Artificial Peptide )
     272 <220> FEATURE:
     273 <221> NAME/KEY: MISC_FEATURE
     274 <222> LOCATION: (1)..(1)
     275 <223> OTHER INFORMATION: is absent or is a terminal group of one to four amino acids
     278 <220> FEATURE:
     279 <221> NAME/KEY: MISC_FEATURE
     280 <222> LOCATION: (2)..(2)
     281 <223> OTHER INFORMATION: is 1Nal, 2Nal, Beta-Asp (Ind), Gly, Tyr, (D)- or (L)-Ala, or
(D
     282         )- or (L)-Phe
     285 <220> FEATURE:
     286 <221> NAME/KEY: MISC_FEATURE
     287 <222> LOCATION: (3)..(4)
     288 <223> OTHER INFORMATION: may be absent, or are independently Gly, Tyr, 1Nal, 2Nal,
Beta-As
     289         p (Ind), Gly, Tyr, (D)- or (L)-Ala, or (D)- or (L)-Phe
```

see item 5 on Error summary Sheet
variable length invalid

9/6/01

RAW SEQUENCE LISTING
PATENT APPLICATION: **US/09/734,583**

DATE: 09/06/2001
TIME: 15:09:42

Input Set : **A:\87534-3000.txt**
Output Set: **N:\CRF3\09062001\I734583.raw**

```
292 <220> FEATURE:
293 <221> NAME/KEY: MISC_FEATURE
294 <222> LOCATION: (5)..(5)
295 <223> OTHER INFORMATION: (D)- or (L)-Trp
298 <220> FEATURE:
299 <221> NAME/KEY: MISC_FEATURE
300 <222> LOCATION: (6)..(6)
301 <223> OTHER INFORMATION: (D)- or (L)-Lys
304 <220> FEATURE:
305 <221> NAME/KEY: MISC_FEATURE
306 <222> LOCATION: (7)..(7)
307 <223> OTHER INFORMATION: is absent or is Gly, Abu, Cys, Thr, Val, (D)- or (L)-Ala, or
(D)
308        - or (L)-Phe
311 <220> FEATURE:
312 <221> NAME/KEY: MISC_FEATURE
313 <222> LOCATION: (8)..(8)
314 <223> OTHER INFORMATION: is Cys, (D)- or (L)-Ala, or (D)- or (L)-Phe
317 <220> FEATURE:
318 <221> NAME/KEY: MISC_FEATURE
319 <222> LOCATION: (9)..(9)
320 <223> OTHER INFORMATION: is absent or is Val, Thr, 1Nal or 2Nal
323 <400> SEQUENCE: 8
W--> 325 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
326  1                   5
329 <210> SEQ ID NO: 9
330 <211> LENGTH: 7
331 <212> TYPE: PRT
C--> 332 <213> ORGANISM: Artificial Peptide
334 <220> FEATURE:
335 <221> NAME/KEY: MISC_FEATURE
336 <222> LOCATION: (1)..(1)
337 <223> OTHER INFORMATION: (D)- or (L)-Phe, Tyr or (D)- or (L)-Ala; Residue 1 is
connected
338        to Residue 7 by a bridge comprised of 1 to 5 methylene spacers co Connected
339        nnected to an amide, thioether, thioester, or disulfide, followe
340        d by 1 to 5 methylene spacers
343 <220> FEATURE:
344 <221> NAME/KEY: MISC_FEATURE
345 <222> LOCATION: (2)..(2)
346 <223> OTHER INFORMATION: (D)- or (L)-Phe, Tyr or (D)- or (L)-Ala;
349 <220> FEATURE:
350 <221> NAME/KEY: MISC_FEATURE
351 <222> LOCATION: (3)..(3)
352 <223> OTHER INFORMATION: is absent or is (D)- or (L)-Phe, Tyr or (D)- or (L)-Ala;
355 <220> FEATURE:
356 <221> NAME/KEY: MISC_FEATURE
357 <222> LOCATION: (4)..(4)
358 <223> OTHER INFORMATION: is (D)- or (L)Tyr
361 <220> FEATURE:
362 <221> NAME/KEY: MISC_FEATURE
```

Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or **Xaa.**

9/6/01

VERIFICATION SUMMARY
PATENT APPLICATION: **US/09/734,583**

DATE: 09/06/2001
TIME: 15:09:43

Input Set : **A:\87534-3000.txt**
Output Set: **N:\CRF3\09062001\I734583.raw**

```
L:30 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2
L:33 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2
L:54 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3
L:83 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4
L:98 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:118 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5
L:121 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:154 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6
L:212 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:219 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7
L:263 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:270 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8
L:325 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:332 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9
L:381 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:388 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10
L:437 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
```

SERIAL NUMBER	FILING DATE		FIRST NAMED APPLICANT	ATTORNEY DOCKET NO.

EXAMINER

ART UNIT	PAPER NUMBER

DATE MAILED:

Please find below a communication from the EXAMINER in charge of this application

Commissioner of Patents

1.   This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 CFR 1.821(a)(1) and (a)(2). A computer readable form (CRF) of the sequence listing was submitted. However, the CRF could not be processed by the Scientific and Technical Information Center (STIC) for the reason(s) set forth on the attached CRF Diskette Problem Report. Applicant must comply with the requirements of the sequence rules (37 CFR 1.821 - 1.825) before the application can be examined under 35 U.S.C. §§ 131 and 132.

Applicant is given ONE MONTH from the mailing date of this communication within which to comply with the sequence rules, 37 CFR 1.821 - 1.825. Failure to comply with these requirements will result in ABANDONMENT of the application under 37 CFR 1.821(g). Extensions of time may be obtained by filing a petition accompanied by the extension fee under the provisions of 37 CFR 1.136(a). Direct the reply to the undersigned. Applicant is requested to return a copy of the attached CRF Diskette Problem Report with the reply.

Anish Gupta

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

☐ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).

☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).

☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).

☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."

☒ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).

☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).

☐ 7. Other: _____

Applicant Must Provide:

☒ An initial or <u>substitute</u> computer readable form (CRF) copy of the "Sequence Listing".

☒ An initial or <u>substitute</u> paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.

☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216
For CRF Submission Help, call (703) 308-4212
PatentIn Software Program Support
    Technical Assistance......................................703-287-0200
    To Purchase PatentIn Software......................703-306-2600

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR REPLY

COUNT SHEET FOR SEQUENCE CASES

Serial No.09/734,583_____   **AE**_____

Date of Count_____

Mark only one space below

_____X_____   **(CRFN)** (CRF is unreadable; use CRF Diskette
                Problem Report)

_____   **(CRFD)** (CRF does not comply; use Notice to
              Comply)

_____   **(CRFR)** (CRF required but none submitted;
              use Notice to Comply)

_____   **(bona fide)** (second or subsequent letter to applicant
              reporting bona fide attempt to comply;
              use Notice to Comply and send copy of RSL)

_____   **(non bona fide)** (second or subsequent letter to
              applicant reporting non-bona fide
              attempt to comply; use Notice to
              Comply and send copy of RSL)

Examiner___Anish Gupta_____   GAU___1653